

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Soos, Jeanne M.
 Schiffenbauer, Joel
 Johnson, Howard M.

 (ii) TITLE OF INVENTION: Orally-Administered Interferon-Tau
10 Compositions and Methods

 (iii) NUMBER OF SEQUENCES: 6

 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Dehlinger & Associates
 (B) STREET: 350 Cambridge Ave., Suite 250
 (C) CITY: Palo Alto
 (D) STATE: CA
 (E) COUNTRY: USA
20 (F) ZIP: 94306

 (v) COMPUTER READABLE FORM:

 (A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

 (vi) CURRENT APPLICATION DATA:

 (A) APPLICATION NUMBER:
30 (B) FILING DATE: 15-MAR-1996
 (C) CLASSIFICATION:

 (viii) ATTORNEY/AGENT INFORMATION:

 (A) NAME: Sholtz, Charles K.
35 (B) REGISTRATION NUMBER: 38,615
 (C) REFERENCE/DOCKET NUMBER: 5600-0003

 (ix) TELECOMMUNICATION INFORMATION:

 (A) TELEPHONE: 415-324-0880
40 (B) TELEFAX: 415-324-0960

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
5 (A) LENGTH: 516 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA
10

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
15 (A) ORGANISM: Ovis aries
(B) STRAIN: Domestic
(D) DEVELOPMENTAL STAGE: Blastula (blastocyst)
(F) TISSUE TYPE: Trophectoderm
20 (G) CELL TYPE: Mononuclear trophectoderm cells

(vii) IMMEDIATE SOURCE:
(B) CLONE: oTP-1a

(viii) POSITION IN GENOME:
25 (C) UNITS: bp

(ix) FEATURE:
(A) NAME/KEY: CDS
30 (B) LOCATION: 1..516

(x) PUBLICATION INFORMATION:
(A) AUTHORS: Ott, Troy L
Van Heeke, Gino
Johnson, Howard M
35 Bazer, Fuller W
(B) TITLE: Cloning and Expression in Saccharomyces
cerevisiae of a Synthetic Gene for the Type I
Trophoblast Interferon Ovine Trophoblast
Protein-1:Purification and Antiviral Activity
40 (C) JOURNAL: J. Interferon Res.
(D) VOLUME: 11

(F) PAGES: 357-364

(G) DATE: 1991

(K) RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1 TO 516

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	TGC TAC CTG TCG CGA AAA CTG ATG CTG GAC GCT CGA GAA AAT TTA AAA	48
	Cys Tyr Leu Ser Arg Lys Leu Met Leu Asp Ala Arg Glu Asn Leu Lys	
	1 5 10 15	
10	CTG CTG GAC CGT ATG AAT CGA TTG TCT CCG CAC AGC TGC CTG CAA GAC	96
	Leu Leu Asp Arg Met Asn Arg Leu Ser Pro His Ser Cys Leu Gln Asp	
	20 25 30	
15	CGG AAA GAC TTC GGT CTG CCG CAG GAA ATG GTT GAA GGT GAC CAA CTG	144
	Arg Lys Asp Phe Gly Leu Pro Gln Glu Met Val Glu Gly Asp Gln Leu	
	35 40 45	
	CAA AAA GAC CAA GCT TTC CCG GTA CTG TAT GAA ATG CTG CAG CAG TCT	192
20	Gln Lys Asp Gln Ala Phe Pro Val Leu Tyr Glu Met Leu Gln Gln Ser	
	50 55 60	
	TTC AAC CTG TTC TAC ACT GAA CAT TCT TCG GCC GCT TGG GAC ACT ACT	240
	Phe Asn Leu Phe Tyr Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr	
25	65 70 75 80	
	CTT CTA GAA CAA CTG TGC ACT GGT CTG CAA CAG CAA CTG GAC CAT CTG	288
	Leu Leu Glu Gln Leu Cys Thr Gly Leu Gln Gln Gln Leu Asp His Leu	
	85 90 95	
30	GAC ACT TGC CGT GGC CAG GTT ATG GGT GAA GAA GAC TCT GAA CTG GGT	336
	Asp Thr Cys Arg Gly Gln Val Met Gly Glu Glu Asp Ser Glu Leu Gly	
	100 105 110	
35	AAC ATG GAT CCG ATC GTT ACT GTT AAA AAA TAT TTC CAG GGT ATC TAC	384
	Asn Met Asp Pro Ile Val Thr Val Lys Lys Tyr Phe Gln Gly Ile Tyr	
	115 120 125	
	GAC TAC CTG CAG GAA AAA GGT TAC TCT GAC TGC GCT TGG GAA ATC GTA	432
40	Asp Tyr Leu Gln Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Ile Val	
	130 135 140	

CGC GTT GAA ATG ATG CGG GCC CTG ACT GTG TCG ACT ACT CTG CAA AAA 480
 Arg Val Glu Met Met Arg Ala Leu Thr Val Ser Thr Thr Leu Gln Lys
 145 150 155 160

5 CGG TTA ACT AAA ATG GGT GGT GAC CTG AAT TCT CCG 516
 Arg Leu Thr Lys Met Gly Gly Asp Leu Asn Ser Pro
 165 170

(2) INFORMATION FOR SEQ ID NO:2:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: amino acid sequence of a mature
 20 OvIFNtau protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

25 Cys Tyr Leu Ser Arg Lys Leu Met Leu Asp Ala Arg Glu Asn Leu Lys
 1 5 10 15

Leu Leu Asp Arg Met Asn Arg Leu Ser Pro His Ser Cys Leu Gln Asp
 20 25 30

30 Arg Lys Asp Phe Gly Leu Pro Gln Glu Met Val Glu Gly Asp Gln Leu
 35 40 45

Gln Lys Asp Gln Ala Phe Pro Val Leu Tyr Glu Met Leu Gln Gln Ser
 50 55 60

35

Phe Asn Leu Phe Tyr Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr
 65 70 75 80

40

Leu Leu Glu Gln Leu Cys Thr Gly Leu Gln Gln Gln Leu Asp His Leu
 85 90 95

GGTCAAGTTA TGGGTGAAGA AGACTCTGCT CTCGGGAGAA CCGGTCCAAC GCTAGCTTTG 360
AAGAGATACT TCCAAGGTAT CCACGTTTAC TTGAAGGAAA AGGGTTACTC TGACTGTGCT 420
5 TGGGAAACCG TCGCTCTAGA AATCATGCGT AGCTTCTCTT CTTTGATCAG CTTGCAAGAA 480
AGATTACGTA TGATGGACGG TGACTTGTCTG AGCCCA 516

(2) INFORMATION FOR SEQ ID NO:4:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

15

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

20

(C) INDIVIDUAL ISOLATE: amino acid sequence for a mature
HuIFNtau protein, HuIFNtau1.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

25

Cys Asp Leu Ser Gln Asn His Val Leu Val Gly Arg Lys Asn Leu Arg
1 5 10 15

Leu Leu Asp Glu Met Arg Arg Leu Ser Pro Arg Phe Cys Leu Gln Asp
20 25 30

30

Arg Lys Asp Phe Ala Leu Pro Gln Glu Met Val Glu Gly Gly Gln Leu
35 40 45

35

Gln Glu Ala Gln Ala Ile Ser Val Leu His Glu Met Leu Gln Gln Ser
50 55 60

Phe Asn Leu Phe His Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr
65 70 75 80

40

Leu Leu Glu Gln Leu Arg Thr Gly Leu His Gln Gln Leu Asp Asn Leu
85 90 95

	Asp	Ala	Cys	Leu	Gly	Gln	Val	Met	Gly	Glu	Glu	Asp	Ser	Ala	Leu	Gly	
					100				105						110		
5	Arg	Thr	Gly	Pro	Thr	Leu	Ala	Leu	Lys	Arg	Tyr	Phe	Gln	Gly	Ile	His	
			115					120					125				
	Val	Tyr	Leu	Lys	Glu	Lys	Gly	Tyr	Ser	Asp	Cys	Ala	Trp	Glu	Thr	Val	
			130				135						140				
10	Arg	Leu	Glu	Ile	Met	Arg	Ser	Phe	Ser	Ser	Leu	Ile	Ser	Leu	Gln	Glu	
		145				150					155				160		
	Arg	Leu	Arg	Met	Met	Asp	Gly	Asp	Leu	Ser	Ser	Pro					
					165					170							

15 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 516 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

25 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

30 (vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HuIFNtau3, mature no leader sequence

(ix) FEATURE:

35 (A) NAME/KEY: CDS

(B) LOCATION: 1..516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

	TGT	GAC	CTG	TCT	CAG	AAC	CAC	GTG	CTG	GTT	GGC	AGC	CAG	AAC	CTC	AGG	48
40	Cys	Asp	Leu	Ser	Gln	Asn	His	Val	Leu	Val	Gly	Ser	Gln	Asn	Leu	Arg	
	1				5					10					15		

	CTC CTG GGC CAA ATG AGG AGA CTC TCC CTT CGC TTC TGT CTG CAG GAC	96
	Leu Leu Gly Gln Met Arg Arg Leu Ser Leu Arg Phe Cys Leu Gln Asp	
	20 25 30	
5	AGA AAA GAC TTC GCT TTC CCC CAG GAG ATG GTG GAG GGT GGC CAG CTC	144
	Arg Lys Asp Phe Ala Phe Pro Gln Glu Met Val Glu Gly Gly Gln Leu	
	35 40 45	
10	CAG GAG GCC CAG GCC ATC TCT GTG CTC CAC GAG ATG CTC CAG CAG AGC	192
	Gln Glu Ala Gln Ala Ile Ser Val Leu His Glu Met Leu Gln Gln Ser	
	50 55 60	
15	TTC AAC CTC TTC CAC ACA GAG CAC TCC TCT GCT GCC TGG GAC ACC ACC	240
	Phe Asn Leu Phe His Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr	
	65 70 75 80	
20	CTC CTG GAG CAG CTC CGC ACT GGA CTC CAT CAG CAG CTG GAT GAC CTG	288
	Leu Leu Glu Gln Leu Arg Thr Gly Leu His Gln Gln Leu Asp Asp Leu	
	85 90 95	
25	GAT GCC TGC CTG GGG CAG GTG ACG GGA GAG GAA GAC TCT GCC CTG GGA	336
	Asp Ala Cys Leu Gly Gln Val Thr Gly Glu Glu Asp Ser Ala Leu Gly	
	100 105 110	
30	AGA ACG GGC CCC ACC CTG GCC ATG AAG AGG TAT TTC CAG GGC ATC CAT	384
	Arg Thr Gly Pro Thr Leu Ala Met Lys Arg Tyr Phe Gln Gly Ile His	
	115 120 125	
35	GTC TAC CTG AAA GAG AAG GGA TAT AGT GAC TGC GCC TGG GAA ATT GTC	432
	Val Tyr Leu Lys Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Ile Val	
	130 135 140	
40	AGA CTG GAA ATC ATG AGA TCC TTG TCT TCA TCA ACC AGC TTG CAC AAA	480
	Arg Leu Glu Ile Met Arg Ser Leu Ser Ser Ser Thr Ser Leu His Lys	
	145 150 155 160	
40	AGG TTA AGA ATG ATG GAT GGA GAC CTG AGC TCA CCT	516
	Arg Leu Arg Met Met Asp Gly Asp Leu Ser Ser Pro	
	165 170	

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 172 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Cys Asp Leu Ser Gln Asn His Val Leu Val Gly Ser Gln Asn Leu Arg
1 5 10 15
15 Leu Leu Gly Gln Met Arg Arg Leu Ser Leu Arg Phe Cys Leu Gln Asp
20 25 30
Arg Lys Asp Phe Ala Phe Pro Gln Glu Met Val Glu Gly Gly Gln Leu
35 40 45
20 Gln Glu Ala Gln Ala Ile Ser Val Leu His Glu Met Leu Gln Gln Ser
50 55 60
Phe Asn Leu Phe His Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr
25 65 70 75 80
Leu Leu Glu Gln Leu Arg Thr Gly Leu His Gln Gln Leu Asp Asp Leu
85 90 95
30 Asp Ala Cys Leu Gly Gln Val Thr Gly Glu Glu Asp Ser Ala Leu Gly
100 105 110
Arg Thr Gly Pro Thr Leu Ala Met Lys Arg Tyr Phe Gln Gly Ile His
115 120 125
35 Val Tyr Leu Lys Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Ile Val
130 135 140
Arg Leu Glu Ile Met Arg Ser Leu Ser Ser Ser Thr Ser Leu His Lys
40 145 150 155 160

Arg Leu Arg Met Met Asp Gly Asp Leu Ser Ser Pro
165 170